

PSMA3 (NM_002788.4) - cDNA + Protein - 2026-11-04

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ACTAGTTTGC GGCATCCTGT GGTATAGGGG AAGCGCTCCG GGCCTGGAAT -29
CCCTACGCGT CCCTTTGGGT TTAGCACGAT GAGCTCAATC GGCACTGGGT 22
                            Me tSerSerIle GlyThrGlyT 8

ATGACCTGTC AGCCTCTACA TTCTCTCCTG ACGGAAGAGT TTTTCAAGTT 72
yrAspLeuSe rAlaSerThr PheSerProA spGlyArgVa lPheGlnVal 24

GAATATGCTA TGAAGGCTGT GGAAAATAGT AGTACAGCTA TTGGAATCAG 122
GluTyrAlaM etLysAlaVa lGluAsnSer SerThrAlaI leGlyIleAr 41

ATGCAAAGAT GGTGTTGTCT TTGGGGTAGA AAAATTAGTC CTTTCTAAAC 172
gCysLysAsp GlyValValP heGlyValGl uLysLeuVal LeuSerLysL 58

TTTATGAAGA AGGTTCCAAC AAAAGACTTT TTAATGTTGA TCGGCATGTT 222
euTyrGluGl uGlySerAsn LysArgLeuP heAsnValAs pArgHisVal 74

GGAATGGCAG TAGCAGGTTT GTTGGCAGAT GCTCGTTCTT TAGCAGACAT 272
GlyMetAlaV alAlaGlyLe uLeuAlaAsp AlaArgSerL euAlaAspIl 91

AGCAAGAGAA GAAGCTTCCA ACTTCAGATC TAACTTTGGC TACAACATTC 322
eAlaArgGlu GluAlaSerA snPheArgSe rAsnPheGly TyrAsnIleP 108
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CACTAAAACA TCTTGCAGAC AGAGTGGCCA TGTATGTGCA TGCATATACA 372
roLeuLysHi sLeuAlaAsp ArgValAlaM etTyrValHi sAlaTyrThr 124

CTCTACAGTG CTGTTAGACC TTTTGGCTGC AGTTTCATGT TAGGGTCTTA 422
LeuTyrSerA laValArgPr oPheGlyCys SerPheMetL euGlySerTy 141

CAGTGTGAAT GACGGTGCGC AACTCTACAT GATTGACCCA TCAGGTGTTT 472  N144S A147T
rSerValAsn AspGlyAlaG lnLeuTyrMe tIleAspPro SerGlyValS 158

CATACGGTTA TTGGGGCTGT GCCATCGGCA AAGCCAGGCA AGCTGCAAAG 522
erTyrGlyTy rTrpGlyCys AlaIleGlyL ysAlaArgGl nAlaAlaLys 174

ACGGAAATAG AGAAGCTTCA GATGAAAGAA ATGACCTGCC GTGATATCGT 572
ThrGluIleG luLysLeuGl nMetLysGlu MetThrCysA rgAspIleVa 191

TAAAGAAGTT GCAAAAATAA TTTACATAGT ACATGACGAA GTTAAGGATA 622  Y199C
lLysGluVal AlaLysIleI leTyrIleVa lHisAspGlu ValLysAspL 208

AAGCTTTTGA ACTAGAACTC AGCTGGGTTG GTGAATTAAC TAATGGAAGA 672
ysAlaPheGl uLeuGluLeu SerTrpValG lyGluLeuTh rAsnGlyArg 224

CATGAAATTG TTCCAAAAGA TATAAGAGAA GAAGCAGAGA AATATGCTAA 722  p.R233del
HisGluIleV alProLysAs pIleArgGlu GluAlaGluL ysTyrAlaLy 241

GGAATCTCTG AAGGAAGAAG ATGAATCAGA TGATGATAAT ATGTAACATT *4
sGluSerLeu LysGluGluA spGluSerAs pAspAspAsn MetStop

TACTCCAGCA TCTATTGTAT TTTAAATTTC TACTCCAGTC CAATGTAACT *54
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ATTTAGCCCT GGATTATACA TACTGTCCAA TTTTCATTAA ATTTTTGTCT *104

TATAA

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